BIAS

Bioinformatics Integrated Application Software

BOSC 2004

McGill Centre for Bioinformatics
Outline

• Motivation
• Requirements
• Object-relational system
• Libraries
• Modules
Motivation

- Systems Biology / Integrative Bioinformatics
- Development platform
- Integration
  - data
    - Structural, sequences, interactions, ...
  - Algorithms and statistics
    - pipelining existing algorithms
    - developing new algorithms
    - Large-scale computations (machine learning, data mining)
Requirements

- Central consistent data repository
  - Databases

- Easy to create prototypes
  - Java

- Useable by non-experts
  - GUI library
Bias infrastructure
Object-oriented database

• Save objects “as-is” in the database.

• Very flexible
• Too flexible?
Relational databases

• Force to respect predefined schema and relationships.

• Structure helps to optimize queries, ensure consistency.

• Too much restrictive?
Object-Relational database

- Relational database:
  + Mature and well established
  - Requires a lot of database-specific access code

- Object-oriented databases:
  + Intuitive with Object-Oriented languages
  - More difficult to maintain.

- Object-Relational:
  - Object-based, backed by a relational database
Using Apache's OJB system

- Using the ODMG standard
- Query
  
gene = Gene.getGeneByName("YAL001C");

or

gene = yeast.genes.get("YAL001C");

- Store new objects

new Gene("YAL001C", yeast, sync);

- Update

  gene.setName("TFC3");

  gene.sync();
Bias infrastructure (library)
Bias infrastructure (modules)
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